09786635 Results

SEQ ID NO: 1

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6880	100.0	6880	6	AX253450	AX253450 Sequence
2	6880	100.0	6880	9	HSA012376	AJ012376 Homo sapi
3	6880	100.0	7260	6	AX253452	AX253452 Sequence
4	6879	100.0	9497	6	AX059973	AX059973 Sequence
5	6879	100.0	9497	9	AF165281	AF165281 Homo sapi
6	6875.8	99.9	9741	6	AX127830	AX127830 Sequence
7	6875.8	99.9	9741	6	AX139817	AX139817 Sequence
8	6875.8	99.9	9741	6	AX351038	AX351038 Sequence
9	6875.8	99.9	9854	6	AX127831	AX127831 Sequence
10	6875.8	99.9	9854	6	AX139818	AX139818 Sequence
11	6870.4	99.9	7860	6	AX092594	AX092594 Sequence
12	6865	99.8	9495	6	AX059978	AX059978 Sequence
13	6862.4	99.7	10442	6	AX060713	AX060713 Sequence
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16	6860.8	99.7	10474	6	AX060719	AX060719 Sequence
17	6860.8	99.7	10474	6	AX060721	AX060721 Sequence
18	6860.8	99.7	10474	6	AX060898	AX060898 Sequence
19	6860.8	99.7	10474	6	AX060900	AX060900 Sequence
20	6845.2	99.5	7862	6	AX135712	AX135712 Sequence
21	6760.2	98.3	9593	6	AX059976	AX059976 Sequence
22	6711.6	97.6	6786	9	AB055982	AB055982 Homo sapi
23	5630	81.8	7878	10	MMABC1	X75926 Mus musculu
24	5455.6	79.3	6801	10	AY208182	AY208182 Rattus no
25	4302	62.5	7074	5	AF362377	AF362377 Gallus ga
26	2052.4	29.8	5097	6	BD012346	BD012346 Genes rel
27	2052.4	29.8	5097	6	BD160225	BD160225 Primer fo
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29	1911.6	27.8	7298	9	AF001945	AF001945 Homo sapi

AF165281

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LOCUS       AF165281                9497 bp    mRNA    linear   PRI 17-AUG-1999
DEFINITION  Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA,
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ACCESSION   AF165281
VERSION     AF165281.1  GI:5734100
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9497)
  AUTHORS   Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
            Deleuze,J.F., Brewer,H.B., Duverger,N., Denefle,P. and Assmann,G.
  TITLE     Tangier disease is caused by mutations in the gene encoding
            ATP-binding cassette transporter 1
  JOURNAL   Nat. Genet. 22 (4), 352-355 (1999)
  MEDLINE   99364413
   PUBMED   10431238
REFERENCE   2  (bases 1 to 9497)
  AUTHORS   Rust,S., Rosier,M., Funke,H., Real,J., Amoura,Z., Piette,J.C.,
            Deleuze,J.F., Brewer,H.B., Duverger,N., Denefle,P. and Assmann,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston
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ORIGIN

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Qy         61 TCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 120
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Qy        121 ATGCCCTCTGCAGGAACACTTCCTTGGGTTCAGGGGATTATCTGTAATGCCAACAACCCC 180
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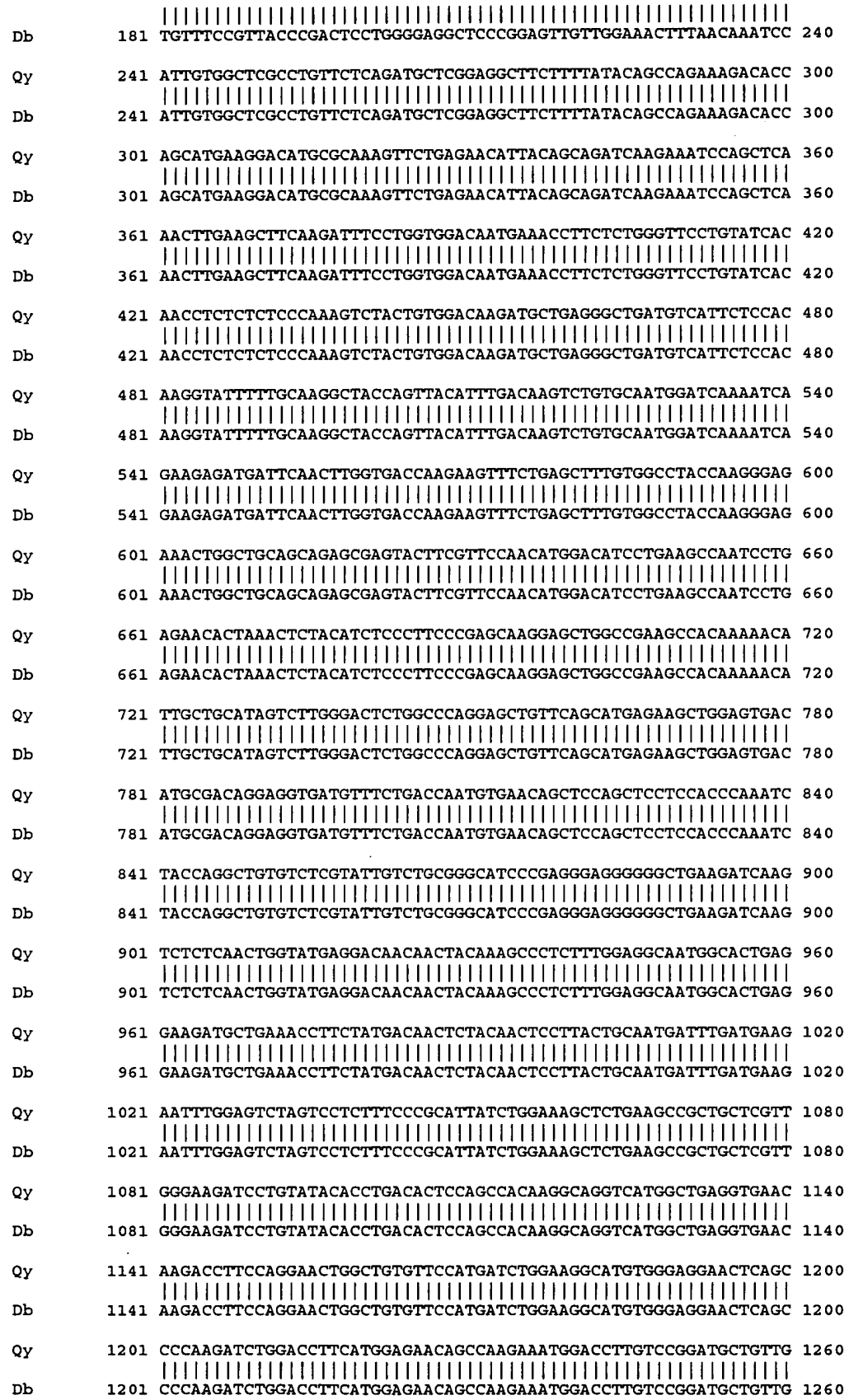

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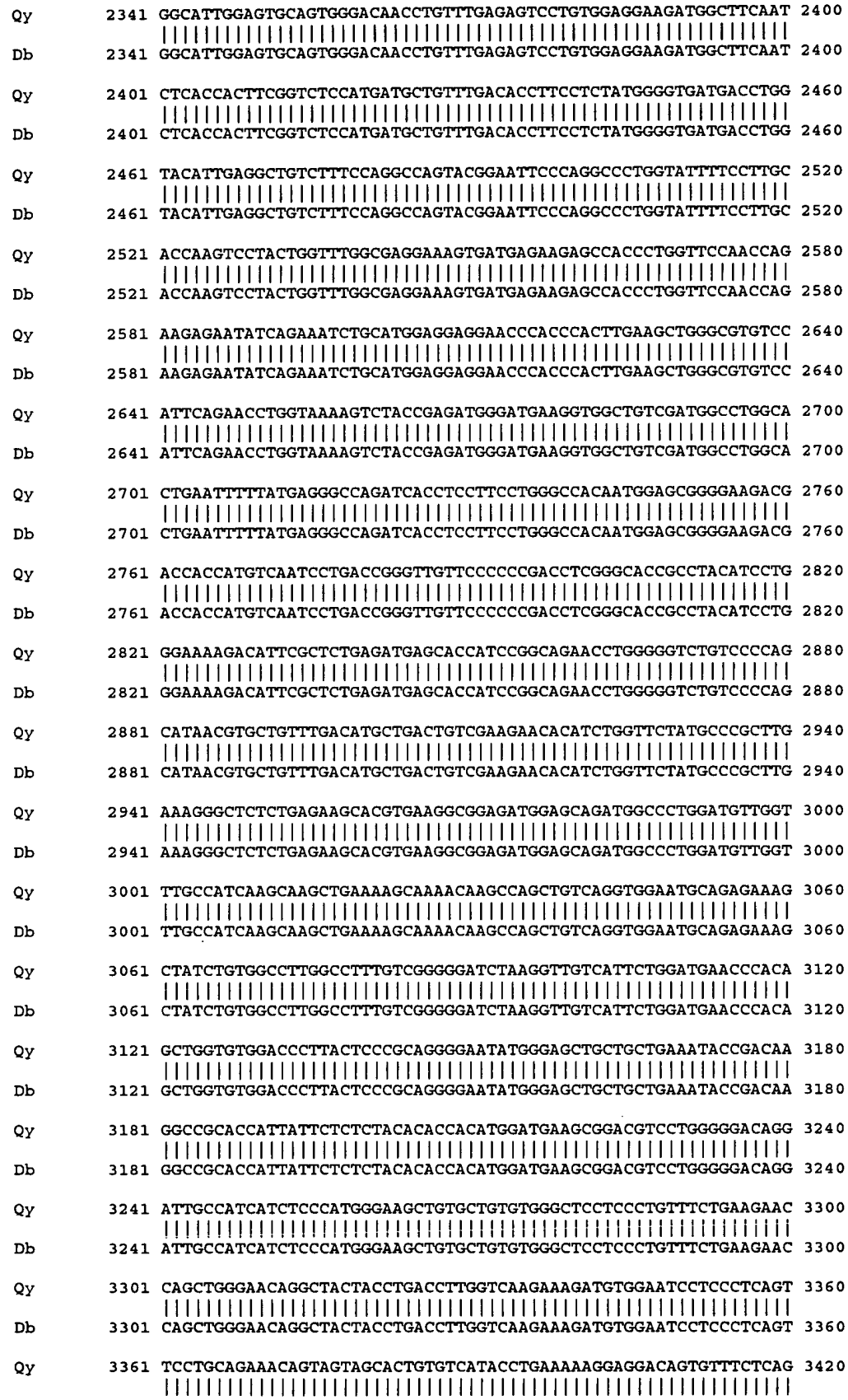

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Qy       4021 GCCCTTGTGTTCAGCCTGATCGTGCCACCCTTTGGCAAGTACCCCAGCCTGGAACTTCAG 4080
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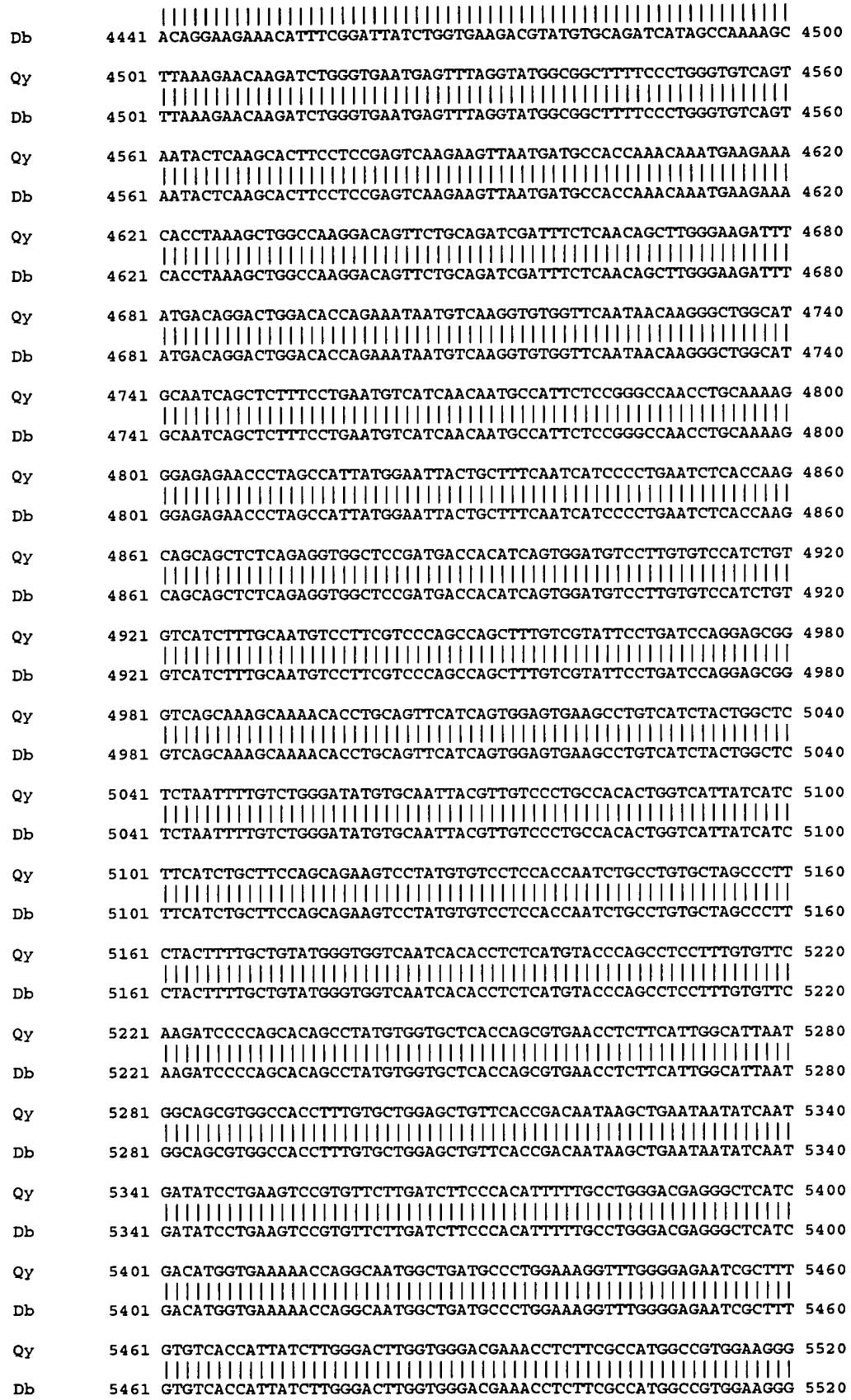

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Db       5881 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG 5940

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Qy       6541 CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT 6600
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Db       6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6880	100.0	6880	21	AAZ94734	Human ATP binding
2	6880	100.0	6880	22	AAI70314	Human ATP binding
3	6880	100.0	7260	22	AAD21326	Human ATP binding
4	6880	100.0	7260	22	AAI70315	Human ATP binding
5	6879	100.0	9497	24	ABV78020	Hypoxia-regulated
6	6876.8	100.0	6880	22	AAD21325	Human ATP binding
7	6875.8	99.9	9741	22	AAS06120	Human ABC1 DNA seq
8	6875.8	99.9	9741	24	AAD37273	Human ABC1 full-le
9	6875.8	99.9	9854	22	AAS06121	Human ABC1 DNA seq
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12	6875.8	99.9	9870	24	ABN99303	Polymorphic human
13	6875.8	99.9	9870	24	ABN99324	Polymorphic human
14	6875.8	99.9	9870	24	ABN99328	Polymorphic human
15	6875.8	99.9	9870	24	ABN99329	Polymorphic human
16	6875.8	99.9	9870	24	ABN99330	Polymorphic human
17	6875.8	99.9	9870	24	ABN99331	Polymorphic human
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20	6875.8	99.9	9870	24	ABN99334	Polymorphic human
21	6875.8	99.9	9870	24	ABN99335	Polymorphic human
22	6875.2	99.9	7281	22	AAK51683	Human polynucleoti
23	6874.2	99.9	9741	24	ABL58146	Human ABCA1 transp
24	6874.2	99.9	9870	24	ABN99304	Polymorphic human
25	6874.2	99.9	9870	24	ABN99305	Polymorphic human
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36	6874.2	99.9	9870	24	ABN99317	Polymorphic human
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44	6874.2	99.9	9870	24	ABN99326	Polymorphic human

45	6874.2	99.9	9870	24	ABN99327	Polymorphic human

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	430.8	6.3	5894	3	US-08-665-259-24	Sequence 24, Appl
2	430.8	6.3	5894	3	US-08-762-500-24	Sequence 24, Appl
3	430.8	6.3	6525	3	US-08-762-500-74	Sequence 74, Appl
4	99.4	1.4	1008	4	US-09-252-991A-4266	Sequence 4266, Ap
c 5	98.8	1.4	999	4	US-09-252-991A-4588	Sequence 4588, Ap
6	89.4	1.3	1614	4	US-09-252-991A-4198	Sequence 4198, Ap
7	85.8	1.2	1824	4	US-09-252-991A-1780	Sequence 1780, Ap
8	83.8	1.2	1176	4	US-09-252-991A-3704	Sequence 3704, Ap
c 9	83.8	1.2	2253	4	US-09-252-991A-3810	Sequence 3810, Ap
10	81	1.2	36181	4	US-08-311-731A-120	Sequence 120, App
11	78.4	1.1	1548	4	US-09-252-991A-3653	Sequence 3653, Ap
c 12	77.4	1.1	762	4	US-09-252-991A-1938	Sequence 1938, Ap
c 13	76.6	1.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
14	75.2	1.1	969	4	US-09-107-532A-1008	Sequence 1008, Ap
15	75	1.1	1770	4	US-09-328-352-3466	Sequence 3466, Ap

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1024.8	14.9	3605	11	AK052916	AK052916 Mus muscu
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4	636.6	9.3	854	12	BI854140	BI854140 603381449
5	624.4	9.1	754	14	CD351847	CD351847 UI-M-GI0-
c 6	591.2	8.6	878	12	BI182779	BI182779 UNL-P-FN-
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c 8	550.4	8.0	661	14	CB481810	CB481810 jns83_A02
9	547.6	8.0	773	14	CB526974	CB526974 UI-M-FY0-
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12	535.2	7.8	702	12	BI658600	BI658600 603284335
13	532.4	7.7	724	12	BG920223	BG920223 602822304
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16	516	7.5	620	14	CA889361	CA889361 B0152D10-
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19	486.4	7.1	605	14	CB546553	CB546553 AMGNNUC:N
20	479.8	7.0	579	14	CA884367	CA884367 B0109G01-
21	477	6.9	1004	11	BC034824	BC034824 Homo sapi
22	473	6.9	562	10	BE665489	BE665489 154542 MA
23	459.4	6.7	515	10	BF094524	BF094524 MR0-UT004
24	456.8	6.6	605	14	CB581583	CB581583 AMGNNUC:N
25	447.6	6.5	554	10	BF076322	BF076322 225856 MA
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RESULT 1
AK051920
LOCUS AK051920 4783 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230019D04 product:ATP-binding cassette, sub-family A (ABC1), member 1, full insert sequence.
ACCESSION AK051920
VERSION AK051920.1 GI:26342297
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4783)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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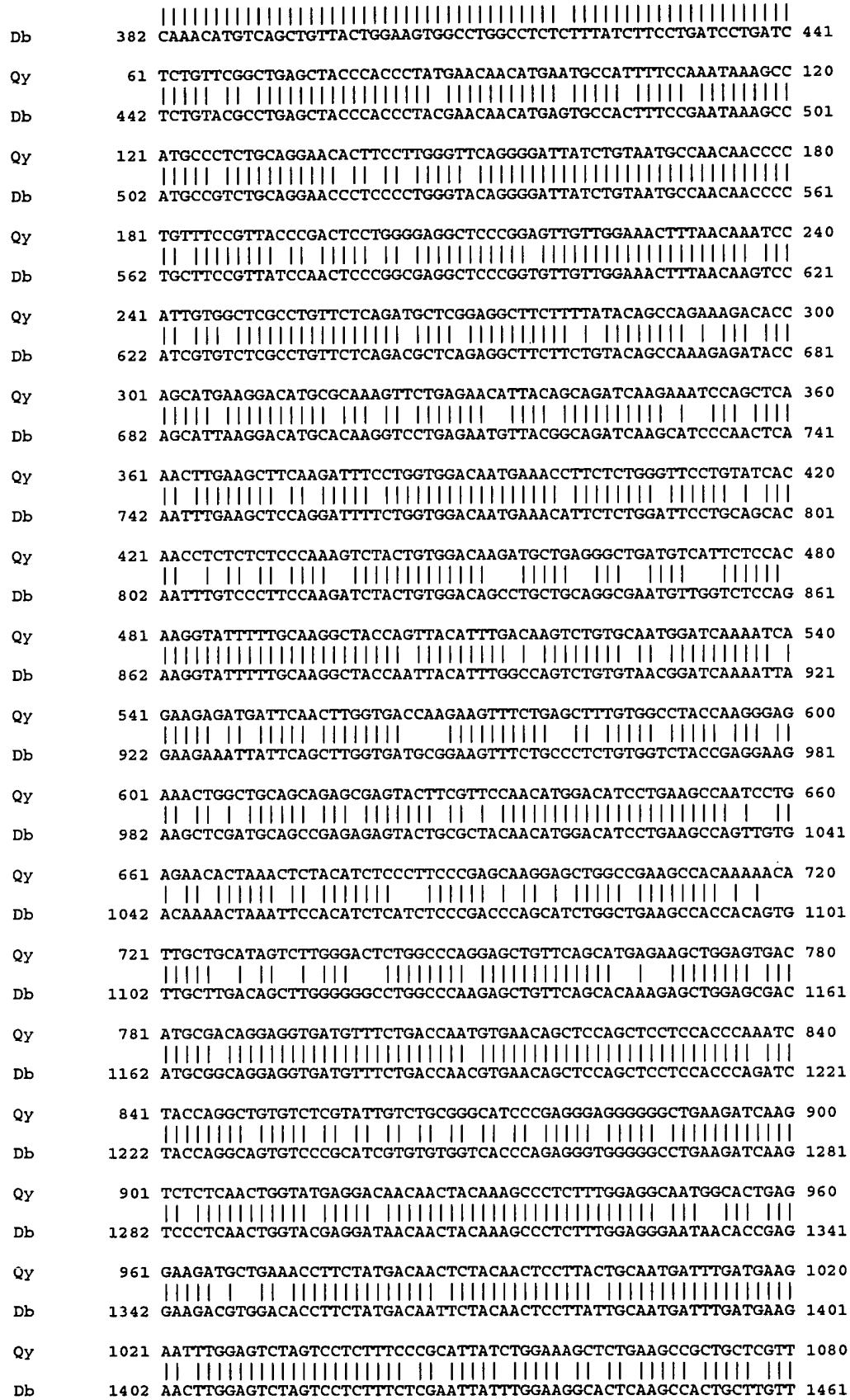

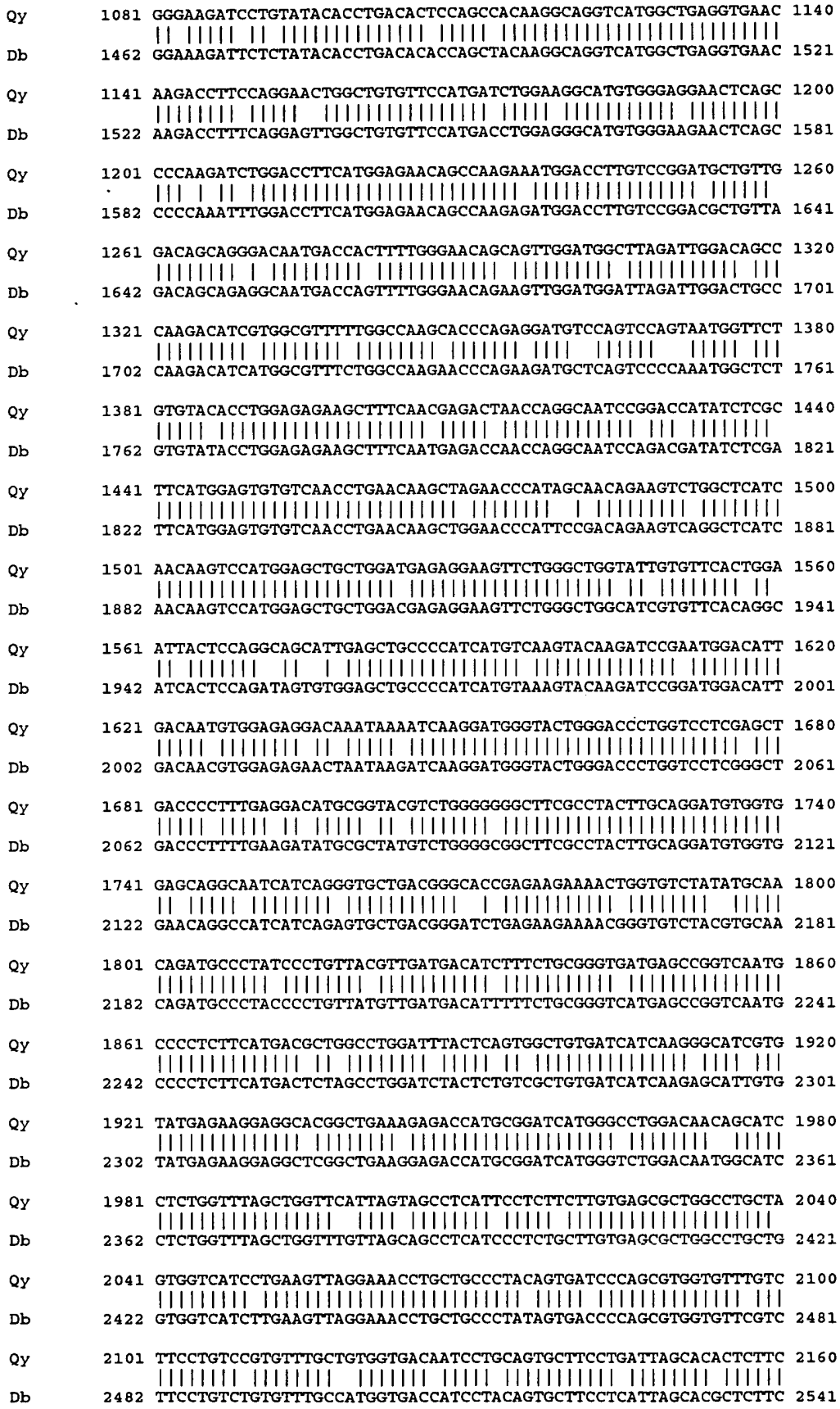
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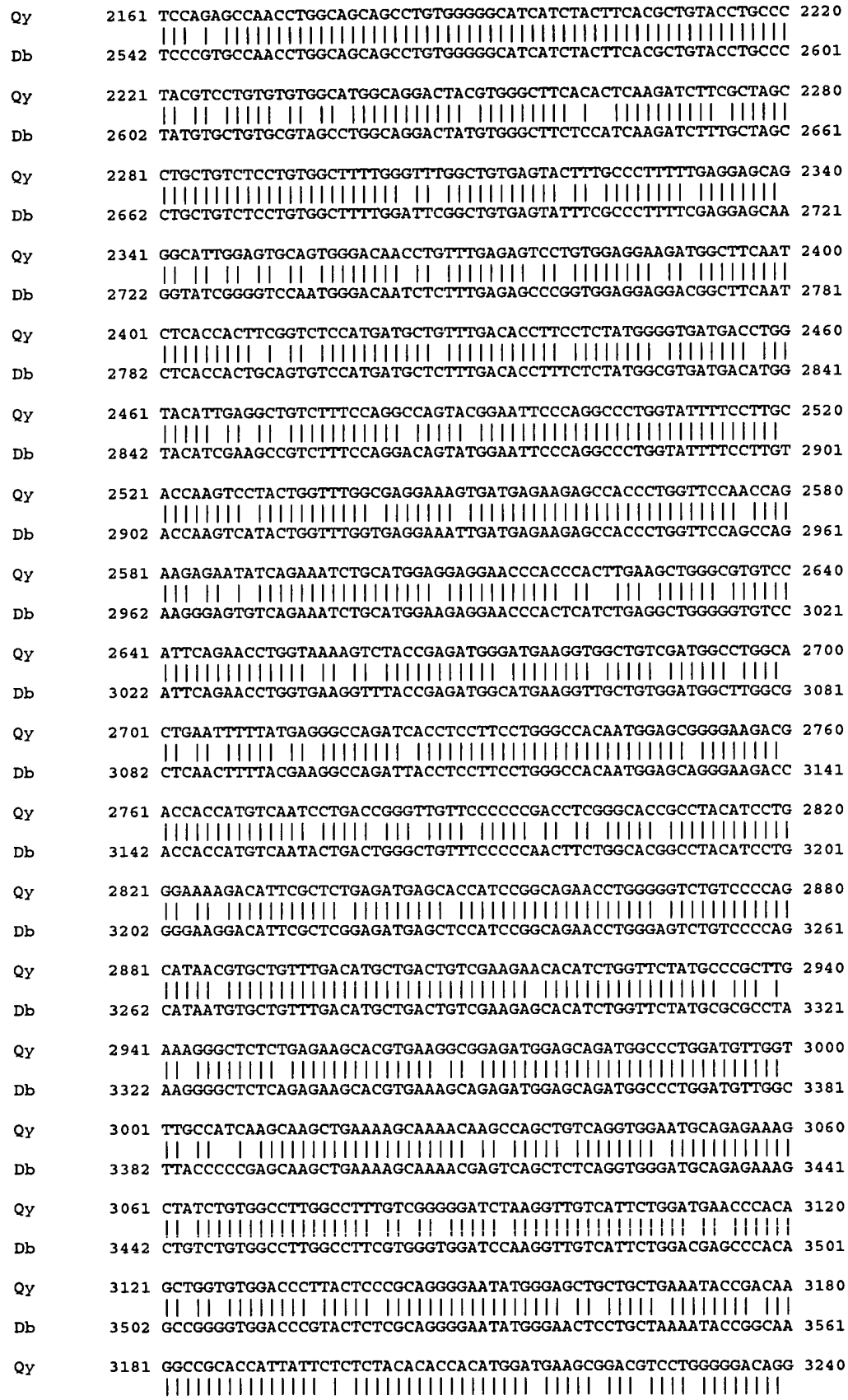

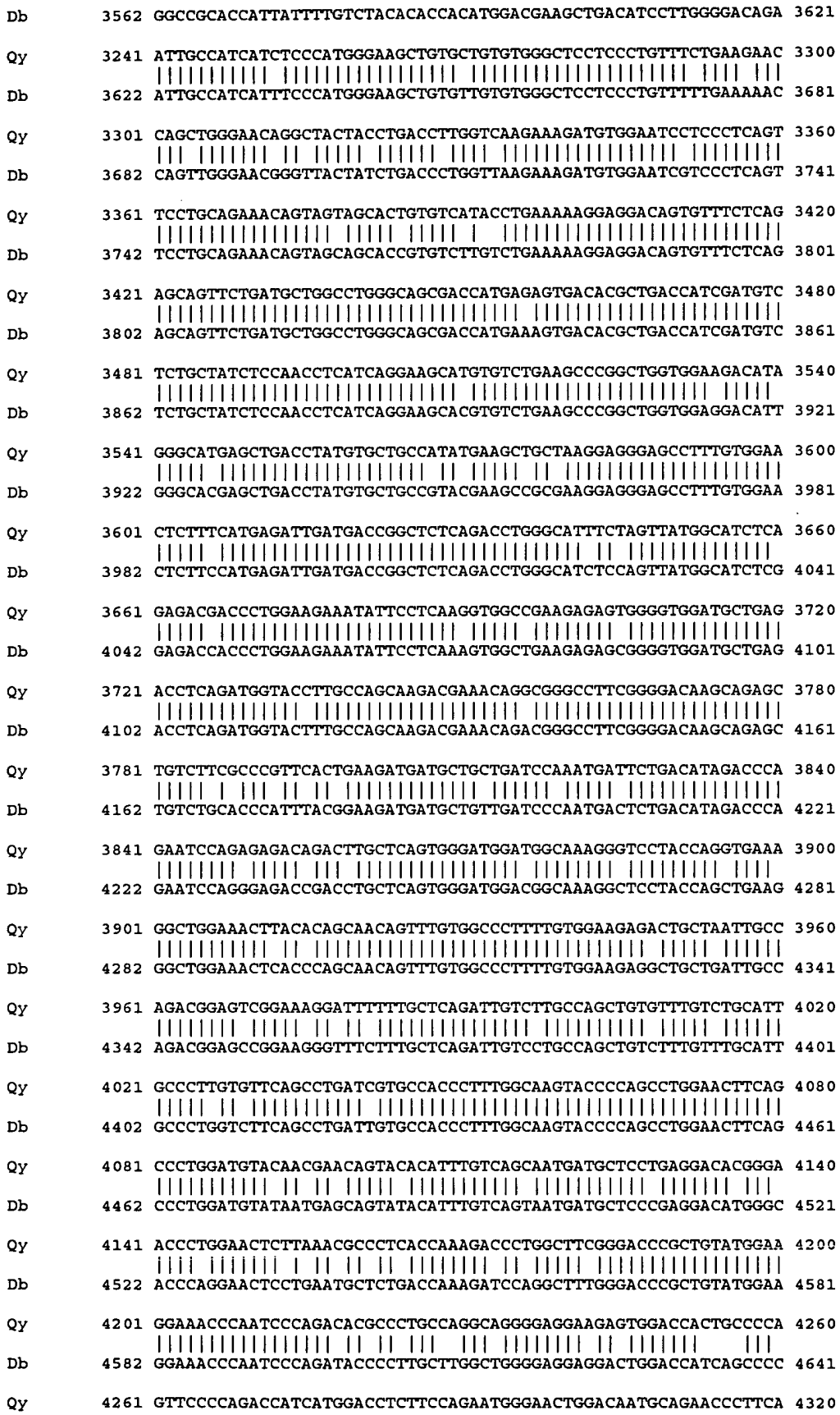
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SEQ ID NO: 2

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29	11459	99.9	2261	23	ABB83118	Polymorphic human
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35	11437	99.7	2261	21	AAB38109	Human ABC1 cholest
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US-08-665-259-26
; Sequence 26, Application US/08665259
; Patent No. 6028173
;  GENERAL INFORMATION:
;    APPLICANT:  Landes, Gregory M.
;    APPLICANT:  Burn, Timothy C.
;    APPLICANT:  Connors, Timothy D.
;    APPLICANT:  Dackowski, William R.
;    APPLICANT:  Van Raay, Terence J.
;    APPLICANT:  Klinger, Katherine W.
;    TITLE OF INVENTION:  NOVEL HUMAN CHROMOSOME 16 GENES,
;    TITLE OF INVENTION:  COMPOSITIONS, METHODS OF MAKING AND USING SAME
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  United States of America
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,259
;      FILING DATE:  17-JUN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  IG5-9.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508) 872-8400
;      TELEFAX:  (508) 872-5415
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1375 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-665-259-26

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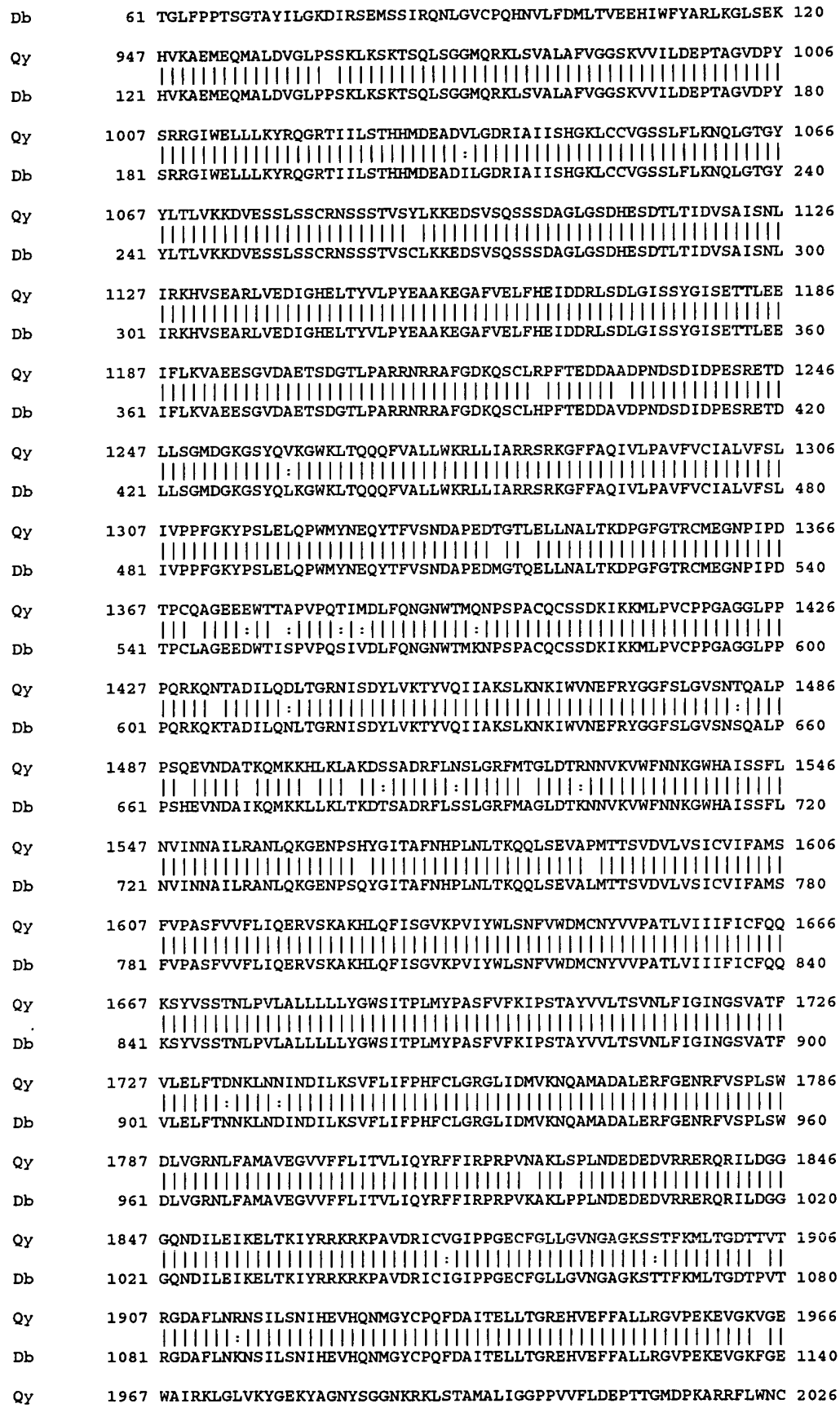
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US-08-762-500-26
; Sequence 26, Application US/08762500
; Patent No. 6030806
;  GENERAL INFORMATION:
;    APPLICANT:  Landes, Gregory M.
;    APPLICANT:  Burn, Timothy C.
;    APPLICANT:  Connors, Timothy D.
;    APPLICANT:  Dackowski, William R.
;    APPLICANT:  Van Raay, Terence J.
;    APPLICANT:  Klinger, Katherine W.
;    TITLE OF INVENTION:  NOVEL HUMAN CHROMOSOME 16 GENES,
;    TITLE OF INVENTION:  COMPOSITIONS, METHODS OF MAKING AND USING SAME
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  One Mountain Road
;      CITY:  Framingham
;      STATE:  Massachusetts
;      COUNTRY:  United States of America
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/762,500
;      FILING DATE:  09-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,259
;      FILING DATE:  17-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10469
;      FILING DATE:  17-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dugan, Deborah A.
;      REGISTRATION NUMBER:  37,315
;      REFERENCE/DOCKET NUMBER:  IG5-9.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508) 872-8400
;      TELEFAX:  (508) 872-5415
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1375 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-762-500-26

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  Best Local Similarity   96.9%;  Pred. No. 0;
  Matches 1332;  Conservative   21;  Mismatches   22;  Indels    0;  Gaps    0;

Qy        827 CMEEEPTHLKLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 886
              |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CMEEEPTHLRLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 60

Qy        887 TGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEK 946
              |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db         61 TGLFPPTSGTAYILGKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEK 120

Qy        947 HVKAEMEQMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 1006
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        121 HVKAEMEQMALDVGLPPSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 180

Qy       1007 SRRGIWELLLKYRQGRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGY 1066
              |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        181 SRRGIWELLLKYRQGRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSLFLKNQLGTGY 240

Qy       1067 YLTLVKKDVESSLSSCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNL 1126
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        241 YLTLVKKDVESSLSSCRNSSSTVSCLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNL 300

Qy       1127 IRKHVSEARLVEDIGHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEE 1186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IRKHVSEARLVEDIGHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEE 360

Qy       1187 IFLKVAEESGVDAETSDGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETD 1246
              |||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db        361 IFLKVAEESGVDAETSDGTLPARRNRRAFGDKQSCLHPFTEDDAVDPNDSDIDPESRETD 420

Qy       1247 LLSGMDGKGSYQVKGWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 1306
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LLSGMDGKGSYQLKGWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 480

Qy       1307 IVPPFGKYPSLELQPWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPD 1366
              |||||||||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db        481 IVPPFGKYPSLELQPWMYNEQYTFVSNDAPEDMGTQELLNALTKDPGFGTRCMEGNPIPD 540

Qy       1367 TPCQAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP 1426
              ||| ||||:|| :||||:|:||||||||||:||||||||||||||||||||||||||||||
Db        541 TPCLAGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 600

Qy       1427 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALP 1486
              ||||| ||||||:||||||||||||||||||||||||||||||||||||||:||||||||
Db        601 PQRKQKTADILQNLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALP 660

Qy       1487 PSQEVNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 1546
              || ||||| ||||| ||| ||:|||||||:|||||| ||||:||||||||||||||||||
Db        661 PSHEVNDAIKQMKKLLKLTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFL 720

Qy       1547 NVINNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMS 1606
              |||||||||||||||||| |||||||||||||||||| ||||||||||||||||||||||
Db        721 NVINNAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMS 780

Qy       1607 FVPASFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQ 1666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 FVPASFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQ 840

Qy       1667 KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 1726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 KSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 900

Qy       1727 VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 1786
              |||||||:||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VLELFTNNKLNDINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 960

Qy       1787 DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1846
              |||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db        961 DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVKAKLPPLNDEDEDVRRERQRILDGG 1020
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Qy       1847 GQNDILEIKELTKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVT 1906
             ||||||||||||||||||||||||||:||||||||||||||||||:|||||||| ||
Db       1021 GQNDILEIKELTKIYRRKRKPAVDRICIGIPPGECFGLLGVNGAGKSTTFKMLTGDTPVT 1080

Qy       1907 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGE 1966
             |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1081 RGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGE 1140

Qy       1967 WAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNC 2026
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1141 WAIRKLGLVKYGEKYASNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNC 1200

Qy       2027 ALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 2086
             |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ALSIVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA 1260

Qy       2087 GSNPDLKPVQDFFGLAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDY 2146
             ||||||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1261 GSNPDLKPVQEFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDY 1320

Qy       2147 SVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 SVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 1375
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10906	95.1	2201	2	A54774	ATP binding casset
2	3338.5	29.1	1529	2	A59189	ATP-binding casset
3	3129.5	27.3	1472	2	B54774	ATP binding casset
4	2638.5	23.0	1704	2	S71363	probable ATP-bindi
5	2635.5	23.0	1704	2	A59188	ATP-binding casset
6	2061	18.0	1802	2	T33783	hypothetical prote
7	1975	17.2	1816	2	A84845	probable ABC trans
8	1854.5	16.2	1447	2	T15200	hypothetical prote
9	1792	15.6	1317	2	C88925	protein F33E11.4 [
10	1535.5	13.4	1758	2	F88559	protein C48B4.4b [
11	1528.5	13.3	1704	2	T42749	ATP-binding casset
12	1526	13.3	1767	2	S60124	transport protein
13	1393	12.1	1246	2	T00826	hypothetical prote
14	1150.5	10.0	1564	2	T27121	hypothetical prote
15	1006.5	8.8	373	2	T47150	hypothetical prote
16	1005.5	8.8	1431	2	T22748	hypothetical prote
17	846	7.4	269	2	T46467	hypothetical prote
18	786.5	6.9	1011	2	T07712	probable ABC-type
19	695	6.1	900	2	T07717	probable ABC-type

```
RESULT 1
A54774
ATP binding cassette transporter ABC1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001
C;Accession: A54774
R;Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimini, G.
Genomics 21, 150-159, 1994
A;Title: Cloning of two novel ABC transporters mapping on human chromosome 9.
A;Reference number: A54774; MUID:94375008; PMID:8088782
A;Accession: A54774
A;Molecule type: mRNA
A;Residues: 1-2201 <LUC>
A;Cross-references: GB:X75926; NID:g495256; PIDN:CAA53530.1; PID:g495257
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; duplication; nucleotide binding; P-loop
F;856-1047/Domain: ATP-binding cassette homology <ABC1>
F;873-880/Region: nucleotide-binding motif A (P-loop)
```

F;1869-2060/Domain: ATP-binding cassette homology <ABC2>
F;1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match 95.1%; Score 10906; DB 2; Length 2201;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

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Qy          1 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDT 60
              ||||||||||||||||||||||||||||||||||||||||:||||||:|||||||:||
Db          1 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVSRLFSDAQRLLLYSQRDT 60

Qy         61 SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH 120
              |:||| |||| |:||| :||||||||||||||||||| ||||||:|||| :|: :| |
Db         61 SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSLPRSTVDSLLQXNVGLQ 120

Qy        121 KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLPREKLAAAERVLRSNMDILKPIL 180
              |||||||||||| ||||||| ||:||||| ||| ||||||:|| ||||||| |||||||::
Db        121 KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRKKLDAAERVLRYNMDILKPVV 180

Qy        181 RTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMRSWSDMRQEVMFLTNVNSSSSSTQI 240
                |||||  |:: |||||  || ||| ||||||| :|||||||||||||||||||||||
Db        181 TKLNSTSHLPTQHLAEATTVLLDSLGGLAQELFSTKSWSDMRQEVMFLTNVNSSSSSTQI 240

Qy        241 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK 300
              |||||||||||||||||||||||||||||||||||| |||| :||||||||||||||||
Db        241 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNNTEEDVDTFYDNSTTPYCNDLMK 300

Qy        301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 360

Qy        361 PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTAQDIVAFLAKHPEDVQSSNGS 420
              |:|||||||||||||| ||||| || ||||:||||||||||:||||||:|||||| |||
Db        361 PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTAQDIMAFLAKNPEDVQSPNGS 420

Qy        421 VYTWREAFNETNQAIRTISRFMECVNLNKLEPIATEVWLINKSMELLDERKFWAGIVFTG 480
              |||||||||||||||:|||||||||||||||||| ||| ||||||||||||||||||||
Db        421 VYTWREAFNETNQAIQTISRFMECVNLNKLEPIPTEVRLINKSMELLDERKFWAGIVFTG 480

Qy        481 ITPGSIELPHHVKYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540
              ||| |:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ITPDSVELPHHVKYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540

Qy        541 EQAIIRVLTGTEKKTGVYMQQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIV 600
              ||||||||||:||||||||:||||||||||||||||||||||||||||||||||||||||
Db        541 EQAIIRVLTGSEKKTGVYVQQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKSIV 600

Qy        601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV 660
              |||||||||||||||||| |||||||:|||||||||||||||||||||||||||||||||
Db        601 YEKEARLKETMRIMGLDNGILWFSWFVSSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV 660

Qy        661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAS 720
              ||||||:|||||||||||||||||||||||||||||||||||||||||||::||||||
Db        661 FLSVFAMVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSIKIFAS 720

Qy        721 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTW 780
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        721 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTAVSMMLFDTFLYGVMTW 780

Qy        781 YIEAVFPGQYGIPRPWYFPCTKSYWFGEESDEKSHPGSNQKRISEICMEEEPTHLKLGVS 840
              |||||||||||||||||||||||||||||| ||||||||:|| :||||||||||||:||||
Db        781 YIEAVFPGQYGIPRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPTHLRLGVS 840

Qy        841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900

Qy        901 GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVG 960
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVG 960
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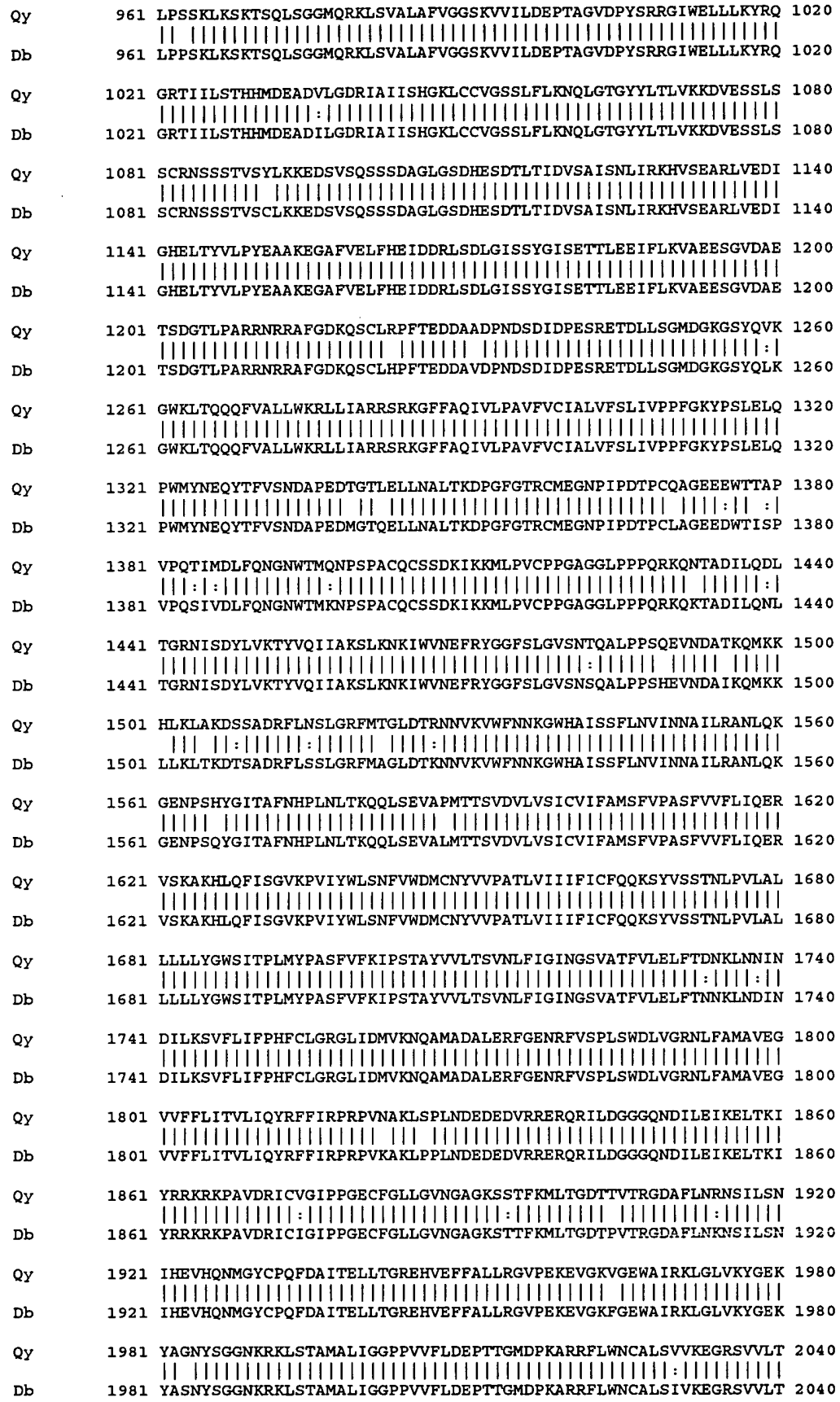
Qy 961 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1020
Db 961 LPPSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1020
Qy 1021 GRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLS 1080
Db 1021 GRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVESSLS 1080
Qy 1081 SCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140
Db 1081 SCRNSSSTVSCLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140
Qy 1141 GHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200
Db 1141 GHELTYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200
Qy 1201 TSDGTLPARRNRRAFGDKQSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVK 1260
Db 1201 TSDGTLPARRNRRAFGDKQSCLHPFTEDDAVDPNDSDIDPESRETDLLSGMDGKGSYQLK 1260
Qy 1261 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1320
Db 1261 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1320
Qy 1321 PWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCMEGNPIPDTPCQAGEEEWTTAP 1380
Db 1321 PWMYNEQYTFVSNDAPEDMGTQELLNALTKDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1380
Qy 1381 VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL 1440
Db 1381 VPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQKTADILQNL 1440
Qy 1441 TGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1500
Db 1441 TGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK 1500
Qy 1501 HLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQK 1560
Db 1501 LLKLTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVINNAILRANLQK 1560
Qy 1561 GENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVVFLIQER 1620
Db 1561 GENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVVFLIQER 1620
Qy 1621 VSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLAL 1680
Db 1621 VSKAKHLQFISGVKPVIYWLSNFVWDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLAL 1680
Qy 1681 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN 1740
Db 1681 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN 1740
Qy 1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
Db 1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
Qy 1801 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
Db 1801 VVFFLITVLIQYRFFIRPRPVKAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
Qy 1861 YRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVTRGDAFLNRNSILSN 1920
Db 1861 YRRKRKPAVDRICIGIPPGECFGLLGVNGAGKSTTFKMLTGDTPVTRGDAFLNKNSILSN 1920
Qy 1921 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGEWAIRKLGLVKYGEK 1980
Db 1921 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGEWAIRKLGLVKYGEK 1980
Qy 1981 YAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT 2040
Db 1981 YASNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSIVKEGRSVVLT 2040

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Qy       2041 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db       2041 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG 2100

Qy       2101 LAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF 2160
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF 2160

Qy       2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
             |||||||||||||||||||||||||||||||||||||||||||
Db       2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11466	100.0	2261	1	ABC1_HUMAN	O95477 homo sapien
2	10906	95.1	2261	1	ABC1_MOUSE	P41233 mus musculu
3	5689.5	49.6	2273	1	ABCR_HUMAN	P78363 homo sapien
4	4131	36.0	2436	1	ABC2_HUMAN	Q9bzc7 homo sapien
5	3989.5	34.8	2434	1	ABC2_MOUSE	P41234 mus musculu
6	2635.5	23.0	1704	1	ABC3_HUMAN	Q99758 homo sapien
7	1528.5	13.3	1704	1	CED7_CAEEL	P34358 caenorhabdi
8	411	3.6	330	1	DRRA_STRPE	P32010 streptomyce
9	380.5	3.3	343	1	NODI_RHISN	P55476 rhizobium s
10	366	3.2	304	1	NODI_RHIS3	P72335 rhizobium s
11	347	3.0	308	1	YADG_ECOLI	P36879 escherichia
12	347	3.0	335	1	NDI2_RHIME	Q8gnh6 rhizobium m
13	344.5	3.0	340	1	NODI_RHILO	P23703 rhizobium l
14	343.5	3.0	347	1	NODI_RHIGA	P50332 rhizobium g
15	335.5	2.9	1280	1	MDR1_HUMAN	P08183 homo sapien
16	331.5	2.9	355	1	NDI1_RHIME	O52618 rhizobium m
17	329.5	2.9	578	1	YBHF_ECOLI	P75776 escherichia
18	327	2.9	894	1	YHIH_ECOLI	P37624 escherichia
19	327	2.9	1276	1	MDR3_MOUSE	P21447 mus musculu

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RESULT 2
ABC1_MOUSE
ID   ABC1_MOUSE     STANDARD;      PRT;  2261 AA.
AC   P41233;
DT   01-FEB-1995 (Rel. 31, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE   transporter 1) (ATP-binding cassette 1) (ABC-1).
GN   ABCA1 OR ABC1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2; TISSUE=Macrophage;
RX   MEDLINE=94375008; PubMed=8088782;
RA   Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT   "Cloning of two novel ABC transporters mapping on human chromosome
RT   9.";
RL   Genomics 21:150-159(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=21251004; PubMed=11352567;
RA   Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT   "Human and mouse ABCA1 comparative sequencing and transgenesis
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RT   studies revealing novel regulatory sequences.";
RL   Genomics 73:66-76(2001).
CC   -!- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
CC       TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
CC       TRANSPORT (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
CC       LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
CC   -!- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC       EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC       ATP BINDING CASSETTE (ABC) DOMAIN.
CC   -!- PTM: Phosphorylation on Ser-2054 regulates phospholipid efflux (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X75926; CAA53530.1; ALT_INIT.
DR   EMBL; AF287263; AAG39073.1; ALT_INIT.
DR   MGD; MGI:99607; Abca1.
DR   GO; GO:0008203; P:cholesterol metabolism; IDA.
DR   GO; GO:0030301; P:cholesterol transport; IDA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transporter; 2.
DR   SMART; SM00382; AAA; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Phosphorylation.
FT   TRANSMEM     26     42       POTENTIAL.
FT   TRANSMEM    640    656       POTENTIAL.
FT   TRANSMEM    690    706       POTENTIAL.
FT   TRANSMEM    717    733       POTENTIAL.
FT   TRANSMEM    749    765       POTENTIAL.
FT   TRANSMEM    771    787       POTENTIAL.
FT   TRANSMEM   1041   1057       POTENTIAL.
FT   TRANSMEM   1351   1367       POTENTIAL.
FT   TRANSMEM   1661   1677       POTENTIAL.
FT   TRANSMEM   1708   1724       POTENTIAL.
FT   TRANSMEM   1737   1753       POTENTIAL.
FT   TRANSMEM   1775   1791       POTENTIAL.
FT   TRANSMEM   1854   1870       POTENTIAL.
FT   NP_BIND     933    940       ATP (POTENTIAL).
FT   NP_BIND    1946   1953       ATP (POTENTIAL).
FT   MOD_RES    1042   1042       PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT                                SIMILARITY).
FT   MOD_RES    2054   2054       PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT                                SIMILARITY).
FT   CARBOHYD     14     14       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    196    196       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    244    244       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    292    292       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    349    349       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    400    400       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    478    478       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    521    521       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    820    820       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1144   1144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1294   1294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1453   1453       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   CARBOHYD   1499   1499       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1504   1504       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1637   1637       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2044   2044       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2238   2238       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   1567   1568       MISSING (IN REF. 2).
FT   CONFLICT   2024   2024       MISSING (IN REF. 2).
SQ   SEQUENCE   2261 AA;  254011 MW;  FAE62B21FD1D09F9 CRC64;

  Query Match             95.1%;  Score 10906;  DB 1;  Length 2261;
  Best Local Similarity   94.8%;  Pred. No. 0;
  Matches 2087;  Conservative   54;  Mismatches   60;  Indels    0;  Gaps    0;

Qy          1 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDT 60
              ||||||||||||||||||||||||||||||||||||||||||:|||||||:|||||||:||
Db         61 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVSRLFSDAQRLLLYSQRDT 120

Qy         61 SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH 120
              |:||| |||| |:|||  :|||||||||||||||||| ||||||:|||| :|: :| |
Db        121 SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSLPRSTVDSLLQXNVGLQ 180

Qy        121 KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLPREKLAAAERVLRSNMDILKPIL 180
              |||||||||||| ||||||| ||:||||| ||| ||||||:|| ||||||| |||||||::
Db        181 KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRKKLDAAERVLRYNMDILKPVV 240

Qy        181 RTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMRSWSDMRQEVMFLTNVNSSSSSTQI 240
                |||||  |:: |||||  || ||| ||||||| :|||||||||||||||||||||||
Db        241 TKLNSTSHLPTQHLAEATTVLLDSLGGLAQELFSTKSWSDMRQEVMFLTNVNSSSSSTQI 300

Qy        241 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK 300
              |||||||||||||||||||||||||||||||||||| |||| :||||||||||||||||
Db        301 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNNTEEDVDTFYDNSTTPYCNDLMK 360

Qy        301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 420

Qy        361 PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTAQDIVAFLAKHPEDVQSSNGS 420
              |:|||||||||||||| ||||| || ||||:||||||||||:||||||:|||||| |||
Db        421 PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTAQDIMAFLAKNPEDVQSPNGS 480

Qy        421 VYTWREAFNETNQAIRTISRFMECVNLNKLEPIATEVWLINKSMELLDERKFWAGIVFTG 480
              |||||||||||||||:|||||||||||||||| ||| ||||||||||||||||||||||
Db        481 VYTWREAFNETNQAIQTISRFMECVNLNKLEPIPTEVRLINKSMELLDERKFWAGIVFTG 540

Qy        481 ITPGSIELPHHVKYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 540
              ||| |:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ITPDSVELPHHVKYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV 600

Qy        541 EQAIIRVLTGTEKKTGVYMQQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIV 600
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        601 EQAIIRVLTGSEKKTGVYVQQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKSIV 660

Qy        601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV 660
              |||||||||||||||||| ||||||||:|||||||||||||||||||||||||||||||||
Db        661 YEKEARLKETMRIMGLDNGILWFSWFVSSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV 720

Qy        661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAS 720
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||::|||||
Db        721 FLSVFAMVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFSIKIFAS 780

Qy        721 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTW 780
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        781 LLSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTAVSMMLFDTFLYGVMTW 840

Qy        781 YIEAVFPGQYGIPRPWYFPCTKSYWFGEESDEKSHPGSNQKRISEICMEEEPTHLKLGVS 840
              |||||||||||||||||||||||||||||| ||||||||:|| :||||||||||||:||||
Db        841 YIEAVFPGQYGIPRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPTHLRLGVS 900

Qy        841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900
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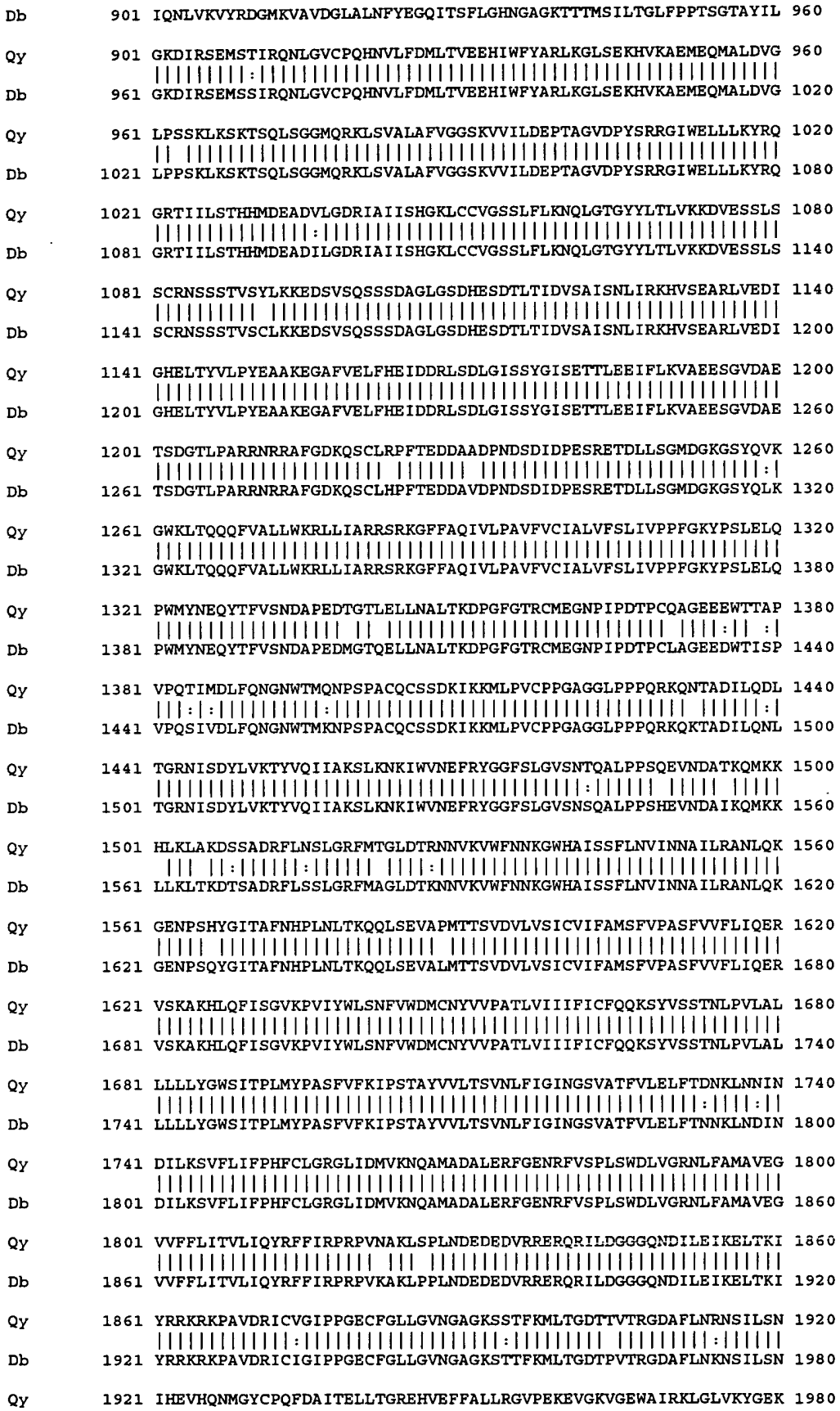

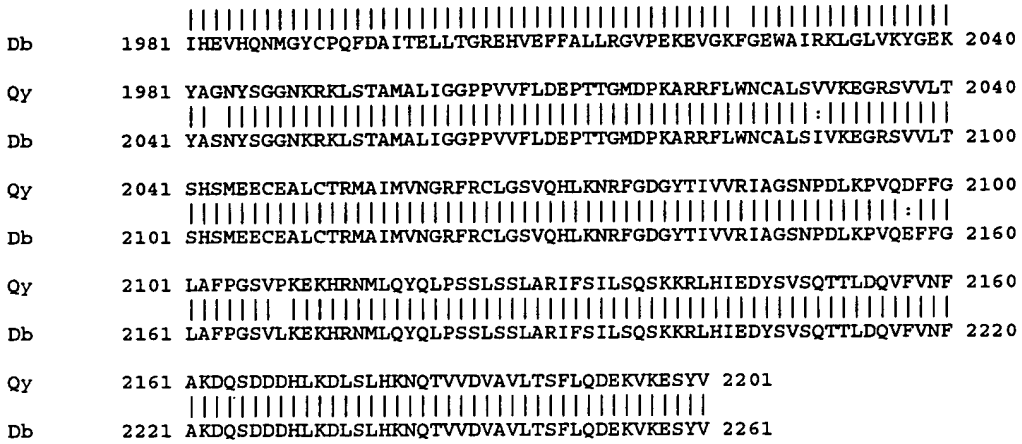
Db 1981 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGEWAIRKLGLVKYGEK 2040
Qy 1981 YAGNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT 2040
Db 2041 YASNYSGGNKRKLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSIVKEGRSVVLT 2100
Qy 2041 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG 2100
Db 2101 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG 2160
Qy 2101 LAFPGSVPKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF 2160
Db 2161 LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFVNF 2220
Qy 2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
Db 2221 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2261